

SEQUENCE LISTING

<110> Dale, James B.

<120> GROUP A STREPTOCOCCAL VACCINES

<130> 481112.410D1

<140> US

<141> 2004-01-16

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

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<212> DNA

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

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<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
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type 5 M protein DNA

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<210> 4

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<212> DNA

<213> Artificial Sequence

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 type 5 M protein DNA

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 type 6 M protein DNA

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 type 6 M protein DNA

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 type 19 M protein DNA

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<210> 8
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 type 1 M protein DNA

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<210> 10
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 type 1 M protein DNA

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<210> 11
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 type 3 M protein DNA

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<210> 12
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 type 3 M protein DNA

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<223> Description of Artificial Sequence: Product of
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type 24 M protein DNA

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<211> 33

<212> DNA

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

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<212> DNA

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<223> Description of Artificial Sequence: Hexavalent M
fusion gene sequence constructed from
streptococcal type 24, 5, 6, 19, 1 and 3 M protein
DNAs

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<221> CDS

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1 5 10 15

caa gaa cgt gct gac aag ttt gag ata gaa aac aat acg tta aaa ctt 96
Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu
20 25 30

aag aat agt gac tta agt ttt aat aat aaa gcg tta aaa gat cat aat 144
Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn
35 40 45

gat gag tta act gaa gag ttg agt aat gct aaa gag aaa cta cgt gga 192
Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly
50 55 60

tcc gcc gtg act agg ggt aca ata aat gac ccg caa aga gca aaa gaa 240
Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu
65 70 75 80

gct ctt gac aag tat gag cta gaa aac cat gac tta aaa act aag aat 288

Ala	Leu	Asp	Lys	Tyr	Glu	Leu	Glu	Asn	His	Asp	Leu	Lys	Thr	Lys	Asn	
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gaa	ggg	tta	aaa	act	gag	aat	gaa	ggg	tta	aaa	act	gag	aat	gaa	ggg	336
Glu	Gly	Leu	Lys	Thr	Glu	Asn	Glu	Gly	Leu	Lys	Thr	Glu	Asn	Glu	Gly	
			100					105					110			
tta	aaa	act	gag	aat	gaa	ggg	tta	aaa	act	gag	gtc	gac	aga	gtg	ttt	384
Leu	Lys	Thr	Glu	Asn	Glu	Gly	Leu	Lys	Thr	Glu	Val	Asp	Arg	Val	Phe	
		115					120					125				
cct	agg	ggg	acg	gta	gaa	aac	ccg	gac	aaa	gca	cga	gaa	ctt	ctt	aac	432
Pro	Arg	Gly	Thr	Val	Glu	Asn	Pro	Asp	Lys	Ala	Arg	Glu	Leu	Leu	Asn	
	130					135					140					
aag	tat	gac	gta	gag	aac	tct	atg	tta	caa	gct	aat	aat	gac	aag	tta	480
Lys	Tyr	Asp	Val	Glu	Asn	Ser	Met	Leu	Gln	Ala	Asn	Asn	Asp	Lys	Leu	
145					150					155					160	
cca	tgg	aga	gtg	cgt	tat	act	agg	cat	acg	cca	gaa	gat	aag	cta	aaa	528
Pro	Trp	Arg	Val	Arg	Tyr	Thr	Arg	His	Thr	Pro	Glu	Asp	Lys	Leu	Lys	
				165					170					175		
aaa	att	att	gac	gat	ctt	gac	gca	aaa	gaa	cat	gaa	tta	caa	caa	cag	576
Lys	Ile	Ile	Asp	Asp	Leu	Asp	Ala	Lys	Glu	His	Glu	Leu	Gln	Gln	Gln	
			180					185					190			
aat	gag	aag	tta	tct	ctg	cag	aac	ggt	gat	ggt	aat	cct	agg	gaa	gtt	624
Asn	Glu	Lys	Leu	Ser	Leu	Gln	Asn	Gly	Asp	Gly	Asn	Pro	Arg	Glu	Val	
		195					200					205				
ata	gaa	gat	ctt	gca	gca	aac	aat	ccc	gca	ata	caa	aat	ata	cgt	tta	672
Ile	Glu	Asp	Leu	Ala	Ala	Asn	Asn	Pro	Ala	Ile	Gln	Asn	Ile	Arg	Leu	
	210					215					220					
cgt	cac	gaa	aac	aag	gac	tta	aaa	gcg	aga	tta	gag	aat	gca	atg	gaa	720
Arg	His	Glu	Asn	Lys	Asp	Leu	Lys	Ala	Arg	Leu	Glu	Asn	Ala	Met	Glu	
225					230					235					240	
gtt	gca	gga	aga	gat	ttt	aag	aga	gct	ggt	acc	ttg	tta	gat	cag	gtt	768
Val	Ala	Gly	Arg	Asp	Phe	Lys	Arg	Ala	Gly	Thr	Leu	Leu	Asp	Gln	Val	
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aca	caa	tta	tat	act	aaa	cat	aat	agt	aat	tac	caa	caa	tat	aat	gca	816
Thr	Gln	Leu	Tyr	Thr	Lys	His	Asn	Ser	Asn	Tyr	Gln	Gln	Tyr	Asn	Ala	
			260					265					270			
caa	gct	ggc	aga	ctt	gac	ctg	aga	caa	aag	gct	gaa	tat	cta	aaa	ggc	864
Gln	Ala	Gly	Arg	Leu	Asp	Leu	Arg	Gln	Lys	Ala	Glu	Tyr	Leu	Lys	Gly	
		275					280					285				
ctt	aat	gat	tgg	gct	gag	agg	ctg	tta	caa	gag	tta	aat	atc	gat	gtc	912
Leu	Asn	Asp	Trp	Ala	Glu	Arg	Leu	Leu	Gln	Glu	Leu	Asn	Ile	Asp	Val	
	290					295					300					
gcg	act	agg	tct	cag	aca	gat	act	ctg	gaa	aaa	gta	caa	gaa	cgt	gct	960
Ala	Thr	Arg	Ser	Gln	Thr	Asp	Thr	Leu	Glu	Lys	Val	Gln	Glu	Arg	Ala	
305					310					315					320	
gac	aag	ttt	gag	ata	gaa	aac	aat	acg	tta	aaa	ctt	aag	aat	agt	gac	1008
Asp	Lys	Phe	Glu	Ile	Glu	Asn	Asn	Thr	Leu	Lys	Leu	Lys	Asn	Ser	Asp	
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tta agt ttt aat aat aaa gcg tta aaa gat cat aat gat gag tta act 1056
Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr
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gaa gag ttg agt aat gct aaa gag aaa cta cgt aaa aat gat aaa tca 1104
Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser
          355          360          365

cta tct gaa aaa gct agt aaa att caa gaa tta gag gca cgt aag 1149
Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys
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taaaagctt 1158

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<210> 16
<211> 383
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Hexavalent M
      fusion gene sequence constructed from
      streptococcal type 24, 5, 6, 19, 1 and 3 M protein
      DNAs

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Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val
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Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn
          35          40          45

Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly
          50          55          60

Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu
          65          70          75          80

Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn
          85          90          95

Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly
          100          105          110

Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe
          115          120          125

Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn
          130          135          140

Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu
          145          150          155          160

Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys
          165          170          175

Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln

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180										185					190						
Asn	Glu	Lys	Leu	Ser	Leu	Gln	Asn	Gly	Asp	Gly	Asn	Pro	Arg	Glu	Val						
		195					200					205									
Ile	Glu	Asp	Leu	Ala	Ala	Asn	Asn	Pro	Ala	Ile	Gln	Asn	Ile	Arg	Leu						
	210					215					220										
Arg	His	Glu	Asn	Lys	Asp	Leu	Lys	Ala	Arg	Leu	Glu	Asn	Ala	Met	Glu						
225					230					235					240						
Val	Ala	Gly	Arg	Asp	Phe	Lys	Arg	Ala	Gly	Thr	Leu	Leu	Asp	Gln	Val						
				245					250					255							
Thr	Gln	Leu	Tyr	Thr	Lys	His	Asn	Ser	Asn	Tyr	Gln	Gln	Tyr	Asn	Ala						
			260					265					270								
Gln	Ala	Gly	Arg	Leu	Asp	Leu	Arg	Gln	Lys	Ala	Glu	Tyr	Leu	Lys	Gly						
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Leu	Asn	Asp	Trp	Ala	Glu	Arg	Leu	Leu	Gln	Glu	Leu	Asn	Ile	Asp	Val						
	290					295						300									
Ala	Thr	Arg	Ser	Gln	Thr	Asp	Thr	Leu	Glu	Lys	Val	Gln	Glu	Arg	Ala						
305					310					315					320						
Asp	Lys	Phe	Glu	Ile	Glu	Asn	Asn	Thr	Leu	Lys	Leu	Lys	Asn	Ser	Asp						
				325					330					335							
Leu	Ser	Phe	Asn	Asn	Lys	Ala	Leu	Lys	Asp	His	Asn	Asp	Glu	Leu	Thr						
			340					345					350								
Glu	Glu	Leu	Ser	Asn	Ala	Lys	Glu	Lys	Leu	Arg	Lys	Asn	Asp	Lys	Ser						
		355					360					365									
Leu	Ser	Glu	Lys	Ala	Ser	Lys	Ile	Gln	Glu	Leu	Glu	Ala	Arg	Lys							
	370					375					380										